TEAM 6

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/726,211

DATE: 11/09/96
TIME: 16:23:16

INPUT SET: S13733.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

1   SEQUENCE LISTING
2
3   (1)   General Information:
4
5   (i) APPLICANT: Tormo, Mar
6   Tari, Ana M.
7   Lopez-Berestein, Gabriel
8
9   (ii) TITLE OF INVENTION: INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY
10   LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES
11
12   (iii) NUMBER OF SEQUENCES: 7
13
14   (iv) CORRESPONDENCE ADDRESS:
15   (A) ADDRESSEE: Arnold, White & Durkee
16   (B) STREET: P.O. Box 4433
17   (C) CITY: Houston
18   (D) STATE: Texas
19   (E) COUNTRY: United States of America
20   (F) ZIP: 77210
21
22   (v) COMPUTER READABLE FORM:
23   (A) MEDIUM TYPE: Floppy disk
24   (B) COMPUTER: IBM PC compatible
25   (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26   (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28   (vi) CURRENT APPLICATION DATA:
--> oK 29   (A) APPLICATION NUMBER: US Unknown
30   (B) FILING DATE: Concurrently Herewith
--> OlC 31   (C) CLASSIFICATION: Unknown
32
33   (viii) ATTORNEY/AGENT INFORMATION:
34   (A) NAME: Wilson, Mark B.
35   (B) REGISTRATION NUMBER: 37,259
36   (C) REFERENCE/DOCKET NUMBER: UTXC:504
37
38   (ix) TELECOMMUNICATION INFORMATION:
39   (A) TELEPHONE: (512) 418-3000
40   (B) TELEFAX: (512) 474-7577
41
42
43   (2) INFORMATION FOR SEQ ID NO:1:
44
45   (i) SEQUENCE CHARACTERISTICS:
46   (A) LENGTH: 18 base pairs

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47              (B) TYPE: nucleic acid
48              (C) STRANDEDNESS: single
49              (D) TOPOLOGY: linear
50
51        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
52
53    CAGCGTGCGC CATCCTTC                                              18
54
55
56    (2) INFORMATION FOR SEQ ID NO:2:
57
58        (i) SEQUENCE CHARACTERISTICS:
59              (A) LENGTH: 20 base pairs
60              (B) TYPE: nucleic acid
61              (C) STRANDEDNESS: single
62              (D) TOPOLOGY: linear
63
64
65        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
66
67    ACGGTCCGCC ACTCCTTCCC                                            20
68
69
70    (2) INFORMATION FOR SEQ ID NO:3:
71
72        (i) SEQUENCE CHARACTERISTICS:
73              (A) LENGTH: 16 base pairs
74              (B) TYPE: nucleic acid
75              (C) STRANDEDNESS: single
76              (D) TOPOLOGY: linear
77
78        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
79
80    CTGAAGGGCT TCTTCC                                                16
81
82
83    (2) INFORMATION FOR SEQ ID NO:4:
84
85        (i) SEQUENCE CHARACTERISTICS:
86              (A) LENGTH: 5086 base pairs
87              (B) TYPE: nucleic acid
88              (C) STRANDEDNESS: single
89              (D) TOPOLOGY: linear
90
91        (ix) FEATURE:
92              (A) NAME/KEY: CDS
93              (B) LOCATION: 1459..2175
94
95        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
96
97    GCGCCCGCCC CTCCGCGCCG CCTGCCCGCC CGCCCGCCGC GCTCCCGCCC GCCGCTCTCC    60
98
99    GTGGCCCCGC CGCGCTGCCG CCGCCGCCGC TGCCAGCGAA GGTGCCGGGG CTCCGGGCCC   120
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101  TCCCTGCCGG CGGCCGTCAG CGCTCGGAGC GAACTGCGCG ACGGGAGGTC CGGGAGGCGA    180
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103  CCGTAGTCGC GCCGCCGCGC AGGACCAGGA GGAGGAGAAA GGGTGCGCAG CCCGGAGGCG    240
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105  GGGTGCGCCG GTGGGGTGCA GCGGAAGAGG GGGTCCAGGG GGGAGAACTT CGTAGCAGTC    300
106
107  ATCCTTTTTA GGAAAAGAGG GAAAAAATAA AACCCTCCCC CACCACCTCC TTCTCCCCAC    360
108
109  CCCTCGCCGC ACCACACACA GCGCGGGCTT CTAGCGCTCG GCACCGGCGG GCCAGGCGCG    420
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111  TCCTGCCTTC ATTTATCCAG CAGCTTTTCG GAAAATGCAT TTGCTGTTCG GAGTTTAATC    480
112
113  AGAAGACGAT TCCTGCCTCC GTCCCCGGCT CCTTCATCGT CCCATCTCCC CTGTCTCTCT    540
114
115  CCTGGGGAGG CGTGAAGCGG TCCCGTGGAT AGAGATTCAT GCCTGTGTCC GCGCGTGTGT    600
116
117  GCGCGCGTAT AAATTGCCGA GAAGGGGAAA ACATCACAGG ACTTCTGCGA ATACCGGACT    660
118
119  GAAAATTGTA ATTCATCTGC CGCCGCCGCT GCCAAAAAAA AACTCGAGCT CTTGAGATCT    720
120
121  CCGGTTGGGA TTCCTGCGGA TTGACATTTC TGTGAAGCAG AAGTCTGGGA ATCGATCTGG    780
122
123  AAATCCTCCT AATTTTTACT CCCTCTCCCC CCGACTCCTG ATTCATTGGG AAGTTTCAAA    840
124
125  TCAGCTATAA CTGGAGAGTG CTGAAGATTG ATGGGATCGT TGCCTTATGC ATTTGTTTTG    900
126
127  GTTTTACAAA AAGGAAACTT GACAGAGGAT CATGCTGTAC TTAAAAAATA CAAGTAAGTC    960
128
129  TCGCACAGGA AATTGGTTTA ATGTAACTTT CAATGGAAAC CTTTGAGATT TTTTACTTAA    1020
130
131  AGTGCATTCG AGTAAATTTA ATTTCCAGGC AGCTTAATAC ATTGTTTTTA GCCGTGTTAC    1080
132
133  TTGTAGTGTG TATGCCCTGC TTTCACTCAG TGTGTACAGG GAAACGCACC TGATTTTTTA    1140
134
135  CTTATTAGTT TGTTTTTTCT TTAACCTTTC AGCATCACAG AGGAAGTAGA CTGATATTAA    1200
136
137  CAATACTTAC TAATAATAAC GTGCCTCATG AAATAAAGAT CCGAAAGGAA TTGGAATAAA    1260
138
139  AATTTCCTGC GTCTCATGCC AAGAGGGAAA CACCAGAATC AAGTGTTCCG CGTGATTGAA    1320
140
141  GACACCCCCT CGTCCAAGAA TGCAAAGCAC ATCCAATAAA ATAGCTGGAT TATAACTCCT    1380
142
143  CTTCTTTCTC TGGGGGCCGT GGGGTGGGAG CTGGGGCGAG AGGTGCCGTT GGCCCCCGTT    1440
144
145  GCTTTTCCTC TGGGAAGG ATG GCG CAC GCT GGG AGA ACG GGG TAC GAC AAC     1491
146                       Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn
147                        1           5                   10
148
149  CGG GAG ATA GTG ATG AAG TAC ATC CAT TAT AAG CTG TCG CAG AGG GGC     1539
150  Arg Glu Ile Val Met Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly
151           15              20                  25
152
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153   TAC GAG TGG GAT GCG GGA GAT GTG GGC GCC GCG CCC CCG GGG GCC GCC        1587
154   Tyr Glu Trp Asp Ala Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala
155            30                  35                  40
156
157   CCC GCA CCG GGC ATC TTC TCC TCC CAG CCC GGG CAC ACG CCC CAT CCA        1635
158   Pro Ala Pro Gly Ile Phe Ser Ser Gln Pro Gly His Thr Pro His Pro
159            45                  50                  55
160
161   GCC GCA TCC CGC GAC CCG GTC GCC AGG ACC TCG CCG CTG CAG ACC CCG        1683
162   Ala Ala Ser Arg Asp Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro
163   60                  65                  70                  75
164
165   GCT GCC CCC GGC GCC GCC GCG GGG CCT GCG CTC AGC CCG GTG CCA CCT        1731
166   Ala Ala Pro Gly Ala Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro
167                     80                  85                  90
168
169   GTG GTC CAC CTG GCC CTC CGC CAA GCC GGC GAC GAC TTC TCC CGC CGC        1779
170   Val Val His Leu Ala Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg
171                95                  100                 105
172
173   TAC CGC GGC GAC TTC GCC GAG ATG TCC AGC CAG CTG CAC CTG ACG CCC        1827
174   Tyr Arg Gly Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro
175                110                 115                 120
176
177   TTC ACC GCG CGG GGA CGC TTT GCC ACG GTG GTG GAG GAG CTC TTC AGG        1875
178   Phe Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg
179                125                 130                 135
180
181   GAC GGG GTG AAC TGG GGG AGG ATT GTG GCC TTC TTT GAG TTC GGT GGG        1923
182   Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly
183   140                 145                 150                 155
184
185   GTC ATG TGT GTG GAG AGC GTC AAC CGG GAG ATG TCG CCC CTG GTG GAC        1971
186   Val Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp
187                     160                 165                 170
188
189   AAC ATC GCC CTG TGG ATG ACT GAG TAC CTG AAC CGG CAC CTG CAC ACC        2019
190   Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr
191                     175                 180                 185
192
193   TGG ATC CAG GAT AAC GGA GGC TGG GAT GCC TTT GTG GAA CTG TAC GGC        2067
194   Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly
195            190                 195                 200
196
197   CCC AGC ATG CGG CCT CTG TTT GAT TTC TCC TGG CTG TCT CTG AAG ACT        2115
198   Pro Ser Met Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr
199            205                 210                 215
200
201   CTG CTC AGT TTG GCC CTG GTG GGA GCT TGC ATC ACC CTG GGT GCC TAT        2163
202   Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr
203   220                 225                 230                 235
204
205   CTG AGC CAC AAG TGAAGTCAAC ATGCCTGCCC CAAACAAATA TGCAAAAGGT           2215
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206   Leu Ser His Lys
207
208
209   TCACTAAAGC AGTAGAAATA ATATGCATTG TCAGTGATGT ACCATGAAAC AAAGCTGCAG   2275
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211   GCTGTTTAAG AAAAAATAAC ACACATATAA ACATCACACA CACAGACAGA CACACACACA   2335
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213   CACAACAATT AACAGTCTTC AGGCAAAACG TCGAATCAGC TATTTACTGC CAAAGGGAAA   2395
214
215   TATCATTTAT TTTTTACATT ATTAAGAAAA AAGATTTATT TATTTAAGAC AGTCCCATCA   2455
216
217   AAACTCCGTC TTTGGAAATC CGACCACTAA TTGCCAAACA CCGCTTCGTG TGGCTCCACC   2515
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219   TGGATGTTCT GTGCCTGTAA ACATAGATTC GCTTTCCATG TTGTTGGCCG GATCACCATC   2575
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221   TGAAGAGCAG ACGGATGGAA AAAGGACCTG ATCATTGGGG AAGCTGGCTT TCTGGCTGCT   2635
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223   GGAGGCTGGG GAGAAGGTGT TCATTCACTT GCATTTCTTT GCCCTGGGGG CGTGATATTA   2695
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225   ACAGAGGGAG GGTTCCCGTG GGGGGAAGTC CATGCCTCCC TGGCCTGAAG AAGAGACTCT   2755
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227   TTGCATATGA CTCACATGAT GCATACCTGG TGGGAGGAAA AGAGTTGGGA ACTTCAGATG   2815
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229   GACCTAGTAC CCACTGAGAT TTCCACGCCG AAGGACAGCG ATGGGAAAAA TGCCCTTAAA   2875
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231   TCATAGGAAA GTATTTTTTT AAGCTACCAA TTGTGCCGAG AAAAGCATTT TAGCAATTTA   2935
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233   TACAATATCA TCCAGTACCT TAAACCCTGA TTGTGTATAT TCATATATTT TGGATACGCA   2995
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235   CCCCCCAACT CCCAATACTG GCTCTGTCTG AGTAAGAAAC AGAATCCTCT GGAACTTGAG   3055
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237   GAAGTGAACA TTTCGGTGAC TTCCGATCAG GAAGGCTAGA GTTACCCAGA GCATCAGGCC   3115
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239   GCCACAAGTG CCTGCTTTTA GGAGACCGAA GTCCGCAGAA CCTACCTGTG TCCCAGCTTG   3175
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241   GAGGCCTGGT CCTGGAACTG AGCCGGGCCC TCACTGGCCT CCTCCAGGGA TGATCAACAG   3235
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243   GGTAGTGTGG TCTCCGAATG TCTGGAAGCT GATGGATGGA GCTCAGAATT CCACTGTCAA   3295
244
245   GAAAGAGCAG TAGAGGGGTG TGGCTGGGCC TGTCACCCTG GGGCCCTCCA GGTAGGCCCG   3355
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247   TTTTCACGTG GAGCATAGGA GCCACGACCC TTCTTAAGAC ATGTATCACT GTAGAGGGAA   3415
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249   GGAACAGAGG CCCTGGGCCT TCCTATCAGA AGGACATGGT GAAGGCTGGG AACGTGAGGA   3475
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251   GAGGCAATGG CCACGGCCCA TTTTGGCTGT AGCACATGGC ACGTTGGCTG TGTGGCCTTG   3535
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253   GCCACCTGTG AGTTTAAAGC AAGGCTTTAA ATGACTTTGG AGAGGGTCAC AAATCCTAAA   3595
254
255   AGAAGCATTG AAGTGAGGTG TCATGGATTA ATTGACCCCT GTCTATGGAA TTACATGTAA   3655
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257   AACATTATCT TGTCACTGTA GTTTGGTTTT ATTTGAAAAC CTGACAAAAA AAAAGTTCCA   3715
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